between the sequences A and C or to the complement (B′) thereof, and detecting the formation of a hybrid of an amplificate and the probe wherein the third sequence (B) located between the binding sequences A and C or the complement (B′) thereof contains no nucleotides that are not part of the sequence section E formed from the binding sequence D of the probe and the sequence of the amplificate bound thereto. The length of the probe is preferably of the same size or larger than the sequence B or the complement B′.

Please replace the paragraph on page 19, line 21 to page 21, line 12 with the following paragraph:

In the first essential step of the method according to the invention a segment of the nucleic acid to be detected is amplified. This segment is also referred to as an amplicon in the following. It is essential that this contains the sequence region between the outer ends of the binding sequences A′ and C of the primers (the primer binding regions) and contains the binding region E of the probe or of the complement thereof. According to the present invention the amplicon (preferably the total length of the sequences of the regions A, B and C) is preferably shorter than 100 nucleotides, particularly preferably shorter than 60 nucleotides, but preferably longer than 40 nucleotides. However, this does not mean that the total length of the amplificates cannot be larger e.g. when the primers have additional nucleotides. Amplification methods are used which allow an amplification of the nucleic acid to be detected or the complement thereof and result in the formation of tripartite mini-nucleic acid amplification products. In principle all nucleic acid amplification methods that are known in
the prior art can be used for this. Target-specific nucleic acid amplification reactions are preferably used. Theoretically exponentional target-specific nucleic acid amplification reactions are particularly preferably used in which an anti-parallel replication of the nucleic acid to be detected or of its complement is carried out e.g. elongation-based reactions such as the polymerase chain reaction (PCR for deoxyribonucleic acids, RT-PCR for ribonucleic acids) or transcription-based reactions such as e.g. nucleic acid sequence based amplification (NASBA) or transcription mediated amplification (TMA). Thermocyclic exponential elongation-based nucleic acid amplification reactions are particularly preferred such as e.g. the polymerase chain reaction. The nucleic acids to be detected or complements thereof which

are used for the amplification can be present in the form of single-stranded or double-stranded deoxyribonucleic acids or ribonucleic acids. The aim of the amplification reaction (amplification) is to produce numerous amplificates of a segment of the nucleic acid to be detected. Hence an amplificate is understood as any molecular species produced by using sequence information of the nucleic acid. In particular the term refers to nucleic acids. The term "amplificate" includes single-stranded as well as double-stranded nucleic acids. In addition to the regions containing the sequence information of the underlying nucleic acid (amplicon), an amplificate can also contain additional regions which are not directly related to sequences of the nucleic acid to be amplified that are outside the ends of the primer binding sites which face away from another. Such sequences with a length of more than 15 nucleotides preferably do not occur on the nucleic acid to be detected or its complement and cannot hybridize with it by direct base pairing. Hence amplificates can either hybridize with the nucleic acid to be detected itself or with its complement. Amplificates are for example also products of an asymmetric amplification i.e. an amplification in which the two strands are formed in different amounts (e.g. by using different amounts of primers) or in which one of the two strands is subsequently destroyed (e.g. by RNase).

Please replace the paragraph on page 25, lines 7 to 18 with the following paragraph:

In the present invention the segment of the nucleic acid from which it is intended to produce a plurality of amplificates is selected such that it contains three regions A, B and C. Regions A and C are regions selected such that one primer can use the complement of sequence A as the binding sequence and the region C can serve as the binding sequence for the other primer. A complement within the sense of the present invention is understood as a nucleic acid or nucleic acid sequence which is essentially complementary to a certain other nucleic acid e.g. a sequence region e.g. of an amplificate or of the nucleic acid to be detected.

Please replace the paragraph on page 41, lines 13 to 16 with the following paragraph:

The primers preferably bind to the binding sequences A′ or C as described above and the probe preferably binds to a region B located between the ends of the binding sequences A′ and C or to the complement thereof.

Please replace the abstract paragraph on page 60, lines 3 to 17 with the following paragraph: